described in ~~copending~~ U.S.S.N. 60/182,296, filed February 14, 2000 (expired), and which is incorporated by reference herein in its entirely for all purposes.

Please replace the paragraph beginning at page 126, lines 16-21, with the following amended paragraph:

All publications and patent documents cited above are hereby incorporated by reference in their entirety for all purposes to the same extent as if each were so individually denoted. Without wishing to exclude incorporating the remainder of the following patent applications, the following sections of the following patent applications are explicitly incorporated by reference herein: Figs 1-8, Table 2, the sequence listing and Examples 1-6 on pages 109-120 of USPN 09/737,246, filed December 13, 2000 (abandoned); Figs 1-8, Table 2, the sequence listing and Examples 1-6 on pages 108-119 of USPN 09/736,969, filed May 7, 2001 (abandoned); Figs. 1-8, Table 2, the sequence listing and Examples 1-4 on pages 106-111 of USPN 09/736,960 filed December 13, 2000 (abandoned); Figs. 1-7, Table 2, the sequence listing and Examples 1-4 on pages 106-111 of USPN 09/736,968, filed December 13, 2000 (abandoned); Figs. 1-9, Table 2, the sequence listing, and Examples 1-7 on pages 106-130 of USPN 09/978,244 filed October 15, 2001 (abandoned); and Figs 1-9, Table 2 and 3, the sequence listing and Examples 1-7 on pages –108-132 of PCT application serial no US02/24482 now published as WO03/025120.

Please replace the paragraph below Example 6B, beginning at page 119, line 7, with the following amended paragraph:

Similar methods have been used to construct fusions for expression of full length hCLASP-2 isoforms as well as truncated C-terminal forms in other cell lines such as Jurkat. Recombinant hCLASP-2 fragments were either isolated by digestion of cDNA clones or amplified by primers flanking specific regions ~~(Please provide some specific regions)~~. These can be cloned into expression vectors such as pBJ1-neo (Mark Davis, Stanford University), Peak12 (B. Seed, Harvard University), and pDsRed1-N1 (Clontech). pBJ1-neo and Peak12 allow untagged expression of recombinant proteins and pDsRed1-N1 will allow either untagged or a C-terminal Red fluorescent protein tag. These can be used to generate protein or for expression of various forms for functional analyses.

Please replace the paragraph beginning at page 120, line 7, with the following amended paragraph:

Media and solutions: RPMI 1640 medium, BioWhitaker; DMEM/M199 medium, BioWhitaker; EMEM, BioWhitaker; Fetal Bovine Serum, Summit (stored frozen at -20°C, stored thawed at 4°C); Trypsin-EDTA, GIBCO ~~(catalogue #25300-054)~~ (stored frozen at -20°C, stored thawed 4°C; Isoton II (stored at RT); DMSO (stored at RT); oligonucleotides (see Table 1 and FIG. 3, stored in solution at -20°C); PBS (Ca^{2+}/Mg^{2+} free); TE; 10 mM Tris-HCL, pH 8.0; 1 mM EDTA.

Please replace the paragraph beginning at page 16, line 18, with the following amended paragraph:

Another preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, 1977, Nuc. Acids Res. 25: 3389-3402 and Altschul *et al.*, 1990, J. Mol. Biol. 215: 403-410, respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence.

Please replace the paragraph beginning on page 7, line 9, with the following amended paragraph:

FIG. 2[[.]]**A.** Schematic of CLASP-2 splice variants. Splice variants are compared to Human (h) CLASP-2A. Numbers above hCLASP-2A line diagram indicate where splice variations comprising deletions and insertions relative to hCLASP-2A are found. Abbreviations: "KIAA" KIAA1058 sequence (Genbank Accession No. AB028981). 2B. Nucleotide and predicted amino acid sequence of CLASP-2A cDNA. Notable protein motifs are